Appendix A: Technical Description of the Stock Synthesis assessment program

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The Stock Synthesis (SS) assessment program provides a statistical framework for calibration of a population dynamics model using a diversity of fishery and survey data. SS is designed to deal with both age- and size-structure with multiple stock sub-areas and multiple growth patterns. The description here details the most commonly applied features, along with a subset of the more advanced options.

1. Population model

The factors described here are those that control the rate at which new individuals recruit to the population each time step; the rate at which they die due to fishing and natural mortality; and the rate at which they grow and contribute to the total biomass and reproductive potential of the stock. The total population can be divided among one to many entities. The total of all entities born within a year are referred to as a year-class or cohort. Each of the biologically- or birth-season-delineated entities is referred to as a morph. In addition, each morph can be sub-divided into slow-, medium-, and fast-growing entities termed platoons (Goodyear, 1997; Taylor and Methot, this volume). The model description here does not include subscripting for morphs or platoons in an attempt for simplicity, but each of these entities is tracked in the population dynamics and biology if the user chooses to invoke these features. Each cohort/morph/platoon is split into males and females if the user invokes a two-gender configuration, and the subscript for gender is included in the description below.

SS can model time-varying processes. Quantities that are time-varying are allowed to change by year and through seasons, and are expressed using a time subscript, t, which is a combination of both year and season. Quantities that are modeled on a yearly time step and are not subject to change over seasons are indicated by a subscript y.

1.1 Initial numbers-at-age

The population in the initial year of a SS application can be simply an unfished equilibrium population, a population in equilibrium with an estimated mortality rate that is influenced by data on historical equilibrium catch, or a population that has estimable age-specific deviations from an equilibrium for a user-specified number of the younger ages.

The numbers of animals of gender γ in age group a in a virgin state (t=0) is:

$$N_{0,\gamma,a} = cR_0 e^{-aM_{\gamma,a}} \quad \text{for } a = 0 \text{ to } 3A-1 \tag{A.1.1}$$

with the plus-group calculated as:

$$N_{0,\gamma,A} = \sum_{a=A}^{3A-1} N_{0,\gamma,a} + \frac{N_{0,\gamma,3A-1}\, e^{-M_{\gamma,a}}}{1-e^{-M_{\gamma,a}}} \tag{A.1.2}$$

where c (I)[1] is a user-defined constant that determines the sex-ratio of recruits[2], $M_{\gamma,a}$ (P)[3] is natural mortality for age a and gender γ, A is the plus-group age, $3A$ is three times the plus-group age, and $R_{0,\gamma}$ is the number of age-0 fish at unfished equilibrium. The plus group virgin

[1] User-specified quantities will henceforth be denoted as "(I)".
[2] The term "recruits" is used to refer to age-0 animals.
[3] Quantities that are directly represented as estimable model parameters will henceforth be denoted as "(P)".

numbers-at-age calculation is based on 3 times the maximum age to include movement dynamics through age 3*A*-1. After calculating the numbers-at-age through age 3*A* in equilibrium, the numbers are collapsed to age *A* for subsequent calculations. Equations A.1.1 and A.1.2 use total mortality, $Z_{t,\gamma,a}$ (see Equation A.1.21), rather than $M_{\gamma,a}$ when the initial equilibrium also involves fishing mortality**.** Although this fishing mortality will reduce spawning biomass, no adjustment is made to R_0 on premise that this reduction has probably not been occurring for enough years to effect this change. R_0 serves as both the starting level of mean recruitment and as the factor that scales the mean spawner-recruitment relationship against which future annual recruitment deviations will act. An estimated offset, R_1, can be applied to R_0 for the initial year only. When the initial population involves age-specific deviations, these deviations are an extension of the zero-centered, lognormal recruitment deviations applied to the equilibrium numbers-at-age (see Equation A.1.7).

1.2 Initial growth

Growth in SS follows the von Bertalanffy function as re-formulated by Schnute (1981), or by the Richards equation which has an option for a 3rd parameter to govern growth. Growth is gender-specific. SS also allows for additional morphs with different growth patterns. Here, we include only the gender-specific formulation for brevity.

Mean size-at-age in SS is calculated from growth parameters at the start of the initial year. The mean size-at-age of each morph is progressed forward according to the growth parameters active during that time period for subsequent seasons within that year and for subsequent years.

The size-at-age in the initial population (*t*=0) is calculated as:

$$\begin{aligned} L_{0,\gamma,a} &= L'_{\min} + ba && \text{for } a \le a_3 \\ L_{0,\gamma,a} &= L_{\infty,\gamma} + \left(L_{1,\gamma} - L_{\infty,\gamma}\right)e^{-k_\gamma(a-a_3)} && \text{for } a > a_3 \text{ to } a = A-1 \end{aligned} \tag{A.1.3}$$

where $L'_{\min}$ (I) is the lower limit of the first population bin, *b* is the linear slope of growth for $a \le a_3$ calculated as:

$$b = \frac{L_{1,\gamma} - L'_{\min}}{a_3} \tag{A.1.4}$$

$L_{0,\gamma,a}$ is the mean size at the start of the equilibrium year for animals of age *a* and gender γ, a_3 (I) is a reference age near the youngest age well-represented in the data, $L_{1,\gamma}$ (P) is the mean size of gender γ at age a_3, k_γ (P) is the growth coefficient for gender γ, and $L_{\infty,\gamma}$ is the mean asymptotic size, calculated from:

$$L_{\infty,\gamma} = L_{1,\gamma} + \frac{L_{2,\gamma} - L_{1,\gamma}}{1 - e^{-k_\gamma(a_4 - a_3)}} \tag{A.1.5}$$

a_4 (I) is a reference age near the oldest age well represented in the data, and $L_{2,\gamma}$ (P) is the mean size of gender γ at age a_4. An option allows $L_{2,\gamma}$ to be used directly as $L_{\infty,\gamma}$.

Growth within the plus-group in the initial year is accounted for by calculating an average length for this group by:

$$L_{0,\gamma,A} = \frac{\sum_{a=A}^{2A} \left(e^{-0.2(a-A+1)}\right) \left(L_{\gamma,A} + \left(\frac{a-A}{A}\right) \left(L_{\infty,\gamma} - L_{0,\gamma,A} \right) \right)}{\sum_{a=A}^{2A} e^{-0.2(a-A+1)}} \tag{A.1.6}$$

This calculation would logically use natural mortality as the decay factor. However, growth is calculated before natural mortality (to allow for size-specific natural mortality, Lorenzen, 1996), so a fixed decay constant of 0.2 is used. Also, A should be large enough such that growth within the plus-group is small.

1.3 Recruitment

The number of age-0 fish is related to spawning biomass according to a stock-recruitment relationship. SS has the option of the Beverton-Holt, Ricker, Hockey-Stick, and a survival-based stock recruitment relationship (Taylor et al., this volume). Here, the Beverton-Holt is described:

$$R_t = \frac{4hR_0 SB_y}{SB_0(1-h) + SB_y(5h-1)} e^{-0.5 b_y \sigma_R^2 + \tilde{R}_y} \qquad \tilde{R}_y \sim N\left(0; \sigma_R^2\right) \tag{A.1.7}$$

where R_0 (P) is the unfished equilibrium recruitment, SB_0 is the unfished equilibrium spawning biomass (corresponding to R_0), SB_y is the spawning biomass at the start of the spawning season during year y, h (P) is the steepness parameter, b_y (I) is the-bias adjustment fraction applied during year y, σ_R (P) is the standard deviation among recruitment deviations in log space, and $\tilde{R}_y$ (P) is the lognormal recruitment deviation for year y. Recruitment is calculated on a yearly basis, but annual recruits can be distributed over seasons and hence the use of the time period subscript t. However, recruitment deviations and bias-adjustments are calculated on an annual basis. The bias-adjustment factor (Methot and Taylor, 2011) ensures unbiased estimation of mean recruitment even during data-poor eras in which the maximum likelihood estimate of $\tilde{R}_y$ is near zero.

The annual bias-adjustment fraction b_y is the piecewise linear function:

$$b_y = \begin{cases} 0 & \text{for } y \le y_1^b \\ b_{\max}\left(1 - \dfrac{y - y_1^b}{y_2^b - y_1^b}\right) & \text{for } y_1^b < y < y_2^b \\ b_{\max} & \text{for } y_2^b \le y \le y_3^b \\ b_{\max}\left(1 - \dfrac{y_3^b - y}{y_4^b - y_3^b}\right) & \text{for } y_3^b < y < y_4^b \\ 0 & \text{for } y_4^b \le y \end{cases} \tag{A.1.8}$$

where y_1^b (I) is the first year of the bias ramp up adjustment period, y_2^b (I) is the last year of the bias ramp up adjustment period, y_3^b (I) is the first year of the bias ramp down adjustment period, y_4^b (I) is the last year of the bias ramp down adjustment period, and $b_{\max}$ (I) is the maximum bias adjustment applied to the recruitment deviations.

The total annual recruitment can be partitioned among growth morphs and birth seasons and areas according to a design matrix. Each of these entities can be further divided into males and females according to a pre-specified fraction. Finally, each of these entities can be further subdivided into platoons that will have slow-, medium- or large-size-at-age relative to the average size-at-age for the overall morph. For morphs that are designated to recruit in a season after the spawning season, their age 0 for the purposes of growth occurs at the start of that season. Thus, they will have smaller size-at-age relative to morphs of that annual cohort that are born earlier, but will grow towards the same L_∞.

1.4 Natural mortality

Natural mortality can take several alternative forms, including age-specific and Lorenzen (Lorenzen, 1996). Further, the parameters which determine natural mortality, in common with those which determine growth, can be time-varying or functions of environmental inputs. The simplest form of natural mortality is:

$$M_{\gamma,a} = \text{constant} \tag{A.1.9}$$

where the natural mortality rate is constant across ages *a* starting at age 0 and equal for genders γ.

1.5 Growth

The mean size-at-age by gender at the start of each season for each growth morph is incremented across season as:

$$L_{t+1,\gamma,a} = L_{t,\gamma,a} + \left(L_{t,\gamma,a-k} - L_{\infty,\gamma}\right)\left(e^{-k_\gamma} - 1\right) \quad \text{for } a < A \tag{A.1.10}$$

The mean size at the start of the season for the plus-group is calculated based on a weighted average of fish moving into the plus-group and existing plus-group fish. This approach allows for a decline in the mean size of fish in the plus-group over time as fishing mortality reduces the numbers in the plus-group. It also prevents an instantaneous change in size of plus-group fish when growth parameters are allowed to be time-varying.

$$L_{t,\gamma,A} = \frac{N_{t,\gamma,A-1}\tilde{L}_{t,\gamma,A} + N_{t,\gamma,A}\left(L_{t,\gamma,A} + \left(L_{t,\gamma,A} + L_{\infty,\gamma}\right)\left(e^{-k_\gamma} - 1\right)\right)}{N_{t,\gamma,A-1} + N_{t,\gamma,A}} \tag{A.1.11}$$

Note that size in the plus-group from Equation A.1.11 will differ slightly from size in the plus-group in the initial year from Equation A.1.6 if fish are still growing appreciably when they reach age *A* and if the mortality factor, 0.2, in Equation A.1.6 is not close to the mortality rate in the application.

Fish of each gender grow according to their current size and current year's *k* and L_∞. Provisions exists for cohort-specific *k* deviations in addition to time-varying *k*, L_∞, and L_1. Cohort-specific growth propagates into forecasts. Fish are not allowed to shrink if L_∞ declines. Another option allows for age-specific k_γ for a user-specified number of younger ages.

The mean size in the middle of the season is calculated from the size at the start of the season as:

$$\tilde{L}_{t,\gamma,a} = L_{t,\gamma,a} + \left(L_{t,\gamma,a} - L_{\infty,\gamma}\right)\left(e^{-0.5(\delta_s)k_\gamma} - 1\right) \qquad \text{(A.1.12)}$$

where δ_s (I) is the duration of season s.

1.6 Variation in size-at-age

Variation in size-at-age can be a function of age or mean length-at-age, with the option of either having the parameters for each gender expressed in terms of the coefficient of variation or the standard deviation. For example, the standard deviation of length-at-age for each gender γ when the coefficient of variation in length changes linearly with size-at-age between parameters specified for ages a_3 and a_4 for each gender γ is given by:

$$\sigma_{t,\gamma,a} = \begin{cases} \tilde{L}_{t,\gamma,a}\left(CV_{1,\gamma}\right) & \text{for } a \le a_3 \\ \tilde{L}_{t,\gamma,a}\left(CV_{1,\gamma} + \dfrac{\left(\tilde{L}_{t,\gamma,a} - L_{1,\gamma}\right)}{\left(L_{2,\gamma} - L_{1,\gamma}\right)}\left(CV_{2,\gamma} - CV_{1,\gamma}\right)\right) & \text{for } a_3 < a < a_4 \\ \tilde{L}_{t.\gamma,a}\left(CV_{2,\gamma}\right) & \text{for } a \ge a_4 \end{cases} \qquad \text{(A.1.13)}$$

where $CV_{1,\gamma}$ (P) is the coefficient of variation of length for gender γ at age a_3, and $CV_{2,\gamma}$ (P) is the coefficient of variation of length for gender γ at age a_4.

1.7 Age-length population structure

The numbers-at-age for each growth morph are distributed across the defined length bins following a normal (or lognormal) distribution. The proportion in length bin l for age a and gender γ at time t, is calculated as follows for the normal case:

$$\varphi_{t,\gamma,a,l} = \begin{cases} \Phi\left(\dfrac{L'_{\min} - \tilde{L}_{t,\gamma,a}}{\sigma_{t,\gamma,a}}\right) & \text{for } l = 1 \\ \Phi\left(\dfrac{L'_{l+1} - \tilde{L}_{t,\gamma,a}}{\sigma_{t,\gamma,a}}\right) - \Phi\left(\dfrac{L'_{l} - \tilde{L}_{t,\gamma,a}}{\sigma_{t,\gamma,a}}\right) & \text{for } 1 < l < A_l \\ 1 - \Phi\left(\dfrac{L'_{\max} - \tilde{L}_{t,\gamma,a}}{\sigma_{t,\gamma,a}}\right) & \text{for } l = A_l \end{cases} \qquad \text{(A.1.14)}$$

where Φ is the standard normal cumulative density function, L'_l (I) is the lower limit of length bin l, $L'_{\max}$ (I) is the lower limit of the largest bin, and A_l (I) is the index of largest length bin. The age-length structured population is calculated at the start of each time period to calculate population and spawning biomass, and at the middle of each time period to calculate selectivity-at-age from selectivity-at-length, and expected size composition for any samples collected during that time period. The mid-year size-at-age is still used as an approximation to size-at-age for any samples collected during the year even if the time period is long (annual). For example, an actual fishery may collect biological samples throughout the year while fish are growing, but a survey may collect samples from just a 1-2 month time period. Currently there is no provision in

SS to account for the broader distribution of size-at-age from fishery samples compared to survey samples; use of seasons will reduce this mismatch.

1.8 Body weight

The weight of a fish of gender γ and length *l* is calculated from:

$$w_{\gamma,l} = \Omega_{\gamma,1}\left(L_l'\right)^{\Omega_{\gamma,2}} \quad \text{(A.1.15)}$$

where L_l' (I) is the mid-size of population length bin *l*, $\Omega_{\gamma,1}$ (P) is the gender-specific weight coefficient, and $\Omega_{\gamma,2}$ (P) is the gender-specific weight exponent. The population mean body weight of fish at age is calculated using Equation A.1.15 based on proportions at length from Equation A.1.14. The mean body weight-at-age for each fishery takes length-selectivity into account.

1.9 Maturity and fecundity

Maturity can be calculated by either length or age. Here, maturity at length *l* is shown calculated using a logistic function:

$$Mat_l = \frac{1}{1+e^{\Omega_3(L_l'-\Omega_4)}} \quad \text{(A.1.16)}$$

where Ω_3 (P) is the slope of the maturity logistic function, and Ω_4 (P) is the length-at-50%-maturity. The number of eggs can be either a function of length or body weight. Eggs per kg of female body weight as a function of body weight is calculated as:

$$\mathrm{Eggs}_l = \Omega_5 + w_{\mathrm{fem},l}\Omega_6 \quad \text{(A.1.17)}$$

where Ω_5 (P) is the intercept of eggs at $w_{fem,l=0}$ (P), and Ω_6 (P) is the slope of number of eggs/kg of body weight. Setting these values to (1,0) will result in reproductive output in units of mature female spawning biomass. Fecundity at age *a* is calculated as:

$$f_a = \sum\nolimits_{l=1}^{A_l} \varphi_{\mathrm{fem},a,l}\left(Mat_l\ Eggs_l\ w_{\mathrm{fem},l}\right) \quad \text{(A.1.18)}$$

where $\varphi_{\mathrm{fem},a,l}$ is the age-length transition matrix for female fish by age *a* and length *l*, determined by gender γ = female fish. The reproductive output (spawning biomass) at the start of the spawning season for each year *y* is calculated by:

$$SB_y = \sum\nolimits_{a=0}^{A} N_{t,\mathrm{fem},a}\, f_a \quad \text{(A.1.19)}$$

1.10 Population with fishing mortality

Fishing mortality is modeled using either Pope's mid-season approximation or continuous *F*. With continuous *F*, the number of fish of gender γ in age group *a*, at the start of time period *t* is:

$$N_{t+1,\gamma,a} = \begin{cases} cR_{t+1,0} & \text{if } a = 0 \\ N_{t,\gamma,a-1}e^{-Z_{t,\gamma,a}} & \text{if } 1 \le a \le A-1 \\ N_{t,\gamma,A-1}e^{-Z_{t,\gamma,A-1}} + N_{t,\gamma,A}e^{-Z_{t,\gamma,A}} & \text{if } a = A \end{cases} \quad \text{(A.1.20)}$$

where *c* (I) is the constant determining the female sex ratio, *t* is the season coinciding with the start of year *y*, and $Z_{t,\gamma,a}$ is the total mortality:

$$Z_{t,\gamma,a} = M_{\gamma,a} + \sum_{f=1}^{A_f} \left(S_{y,f,\gamma,a} F_{t,f} \right) \quad \text{(A.1.21)}$$

where $F_{t,f}$ is the apical fishing mortality rate for time period *t* by fishery *f*, A_f (I) is the number of fisheries, and $S_{y,f,\gamma,a}$ is the gear selectivity for year *y* ($t \in y$) by fishery *f* on animals of age *a* and gender γ.

A hybrid fishing mortality method allows the *F's* to be tuning coefficients to match the input catches nearly exactly, rather than full model parameters. The method begins by calculating the mid-season harvest rate using Pope's approximation. This harvest rate is then converted to an approximation of the Baranov continuous *F*. The *F* values for all fleets operating in that season and area are then tuned over a set number of iterations to match the observed catch for each fleet with its corresponding *F*. Differentiability is achieved by the use of Pope's approximation to obtain the starting value for each *F* and then the use of a fixed number of tuning iterations, typically 4. Tests have shown that modeling *F* as hybrid versus *F* as a parameter has trivial impact on the estimates of the variances of other model derived quantities.

The hybrid method calculates the harvest rate using the Pope's approximation then converts it to an approximation of the corresponding *F* as:

$$\begin{aligned}
temp_{1,t,f} &= \frac{C^{obs}_{t,f,retained}}{B_{t,f} + 0.1 C^{obs}_{t,f,retained}} \\
j_{1,t,f} &= \left(1 + e^{\left(30\left(temp_{1,t,f} - 0.95\right)\right)} \right)^{-1} \\
temp_{2,t,f} &= j_{1,t,f}\, temp_{1,t,f} + 0.95\left(1 - j_{1,t,f}\right) \\
F_{1,t,f} &= \frac{-\ln(1 - temp_{2,t,f})}{\delta_s}
\end{aligned} \quad \text{(A.1.22)}$$

where $C^{obs}_{t,f,retained}$ is the observed retained catch for fishery *f* for time period *t*, δ_s is the duration of the season, and $B_{t,f}$ is the estimated mid-season retained dead biomass for that fleet. Calculations below do not include retention and discard mortality aspects, as well as time-varying selectivity, for simplicity. Equation A1.22 is designed so that high harvest rates (above 0.95) are converted into an *F* that corresponds to a harvest rate of close to 0.95, thus providing a more robust starting point for subsequent iterative adjustment of this *F*. The logistic joiner, *j*, is used at other places in SS to link across discontinuities.

The catch during time period *t*, of gender γ of age *a* fish is:

$$C_{t,\gamma,a} = \sum_f^{A_f} \frac{F_{t,f}}{Z'_{t,\gamma,a}} \left(S_{y,f,\gamma,a} N_{t,\gamma,a} \right) \lambda'_{t,\gamma,a} \quad \text{(A.1.23)}$$

where $Z'_{t,\gamma,a}$ is the adjusted total mortality for time period *t* for gender γ and age *a* (eq. A.1.26), $\lambda'_{t,\gamma,a}$ is the survivorship for time period *t* for gender γ and age *a* (see Eqn A.1.26), and $F_{t,f}$ is the apical fishing mortality rate for time period *t* for fishery *f*.

The survivorship is calculated as:

$$\lambda_{t,\gamma,a} = \left(1 - e^{\left(-\delta_s Z_{t,\gamma,a}\right)}\right) \Big/ Z_{t,\gamma,a} \tag{A.1.24}$$

Total fishing mortality is then adjusted over several fixed number of iterations (typically four, but more in high *F* and multiple fishery situations). The first step is to calculate the ratio of the total observed catch over all fleets to the predicted total catch according to the current *F* estimates. This ratio provides an overall adjustment factor to bring the total mortality closer to what it will be after adjusting the individual *F*s.

$$\begin{aligned} \hat{C}_t &= \sum_{f=1}^{A_f} \sum_{\gamma}^{A_\gamma} \sum_{a=0}^{A} \frac{F_{1,t,f}}{Z_{t,\gamma,a}} \left(w_{\gamma,a} N_{t,\gamma,a} S_{y,f,\gamma,a} \right) \lambda_{t,\gamma,a} \\ Z_t^{adj} &= \frac{C_t^{obs}}{\hat{C}_t + 0.0001} \end{aligned} \tag{A.1.25}$$

where C_t^{obs} is the observed total catch for time period *t* and A_γ (I) is the index of the number of genders.

The total mortality if this adjuster was applied to all the *F*s is then calculated:

$$\begin{aligned} Z'_{t,\gamma,a} &= M_{\gamma,a} + Z^{adj} \left(Z_{t,\gamma,a} - M_{\gamma,a} \right) \\ \lambda'_{t,\gamma,a} &= \left(1 - e^{\left(-\delta_s Z'_{t,\gamma,a}\right)}\right) \Big/ \left(Z'_{t,\gamma,a} \right) \end{aligned} \tag{A.1.26}$$

The adjusted mortality rate is used to calculate the total kill that is retained for each fishery (*temp*$_3$ in eq. A.1.27), and then the new *F* estimate is calculated by the ratio of observed catch to retained kill, with a constraint to prevent unreasonably high *F* calculations:

$$\begin{aligned} temp_{3,t,f} &= \sum_{\gamma=1}^{A_\gamma} \sum_{a=0}^{A} \left(w_{\gamma,a} N_{t,\gamma,a} S_{y,f,\gamma,a} \right) \lambda'_{t,\gamma,a} \\ F_{2,t,f} &= \frac{C^{obs}_{t,f,retained}}{temp_{3,t,f} + 0.0001} \\ j_{2,t,f} &= \left(1 + \exp^{30\left(F_{2,t,f} - 0.95 * F_{\max}\right)} \right)^{-1} \end{aligned} \tag{A.1.27}$$

The updated estimate of *F* for time period *t* is then calculated as:

$$F_{t,f} = j_{2,t,f} F_{2,t,f} + (1 - j_{2,t,f}) F_{\max} \tag{A.1.28}$$

where $F_{\max}$ (I) is the maximum allowable *F*.

1.10 Selectivity

Selectivity is used to define the relationship between the age-length matrix of fish in the population for year *y*, and the expected numbers at age-length that would occur in a sample from the population using a particular fishery or survey. For fisheries, selectivity also describes how fishing mortality is distributed across ages. Many age- and size-selectivity patterns are available in SS. Some take parametric forms, others are non-parametric. The simplest is a basic logistic curve, calculated as:

$$S_{y,f,\gamma,l} = \left(1 + e^{\left(-\ln(19)(L_l' - \beta_{1,y,f,\gamma})/\beta_{2,y,f,\gamma}\right)}\right)^{-1} \tag{A.1.29}$$

where $\beta_{1,y,f,\gamma}$ (P) is the size-at-50%-selectivity for fishery *f* for animals gender γ during year *y*, and $\beta_{2,y,f,\gamma}$ (P) is the difference between the size-at-95% selectivity and that at 50%-selectivity for fishery *f* for animals gender γ during year *y*,. A comparable logistic selectivity function is provided for age selectivity.

The double normal is a more flexible selectivity function, which can create either a dome-shaped or an asymptotic selectivity pattern by length or age through the use of an ascending limb, a plateau and a descending limb. These three components of the overall function are connected by steep logistic "joiners" to provide overall differentiability. Selectivity at minimum and maximum sizes can be directly controlled by parameter specification, for a total of 6 parameters describing the function (Fig. A.1). Selectivity by length *l* is calculated as:

$$S_{y,f,\gamma,l} = asc_{y,f,\gamma,l}(1 - j_{1,y,f,\gamma,l}) + j_{1,y,f,\gamma,l}((1 - j_{2,y,f,\gamma,l}) + j_{2,y,f,\gamma,l}dsc_{y,f,\gamma,l}) \tag{A.1.30}$$

where the joiner functions for the ascending, and descending components are:

$$\begin{aligned} j_{1,y,f,\gamma,l} &= \left(1 + e^{\left(-20\frac{L_l' - \beta_{1,y,f,\gamma}}{1 + \left|L_l' - \beta_{1,y,f,\gamma}\right|}\right)}\right)^{-1} \\ j_{2,y,f,\gamma,l} &= \left(1 + e^{\left(-20\frac{L_l' - peak_{2,y,f,\gamma}}{1 + \left|L_l' - peak_{2,y,f,\gamma}\right|}\right)}\right)^{-1} \end{aligned} \tag{A.1.31}$$

and the ascending and descending limbs when estimating minimum and maximum size at selectivity are:

$$\begin{aligned} asc_{y,f,\gamma,l} &= \left(1 + e^{-\beta_{5,y,f,\gamma}}\right)^{-1} + \left(1 - \left(1 + e^{-\beta_{5,y,f,\gamma}}\right)^{-1}\right)\frac{e^{\left(\frac{-\left(L_l' - \beta_{1,y,f,\gamma}\right)^2}{e^{\beta_{3,y,f,\gamma}}}\right)} - t1_{\min,y,f,\gamma}}{1 - t1_{\min,y,f,\gamma}} \\ dsc_{y,f,\gamma,l} &= 1 + \left(\left(1 + e^{-\beta_{6,y,f,\gamma}}\right)^{-1} - 1\right)\frac{e^{\left(\frac{-\left(L_l' - peak_{2,y,f,\gamma}\right)}{e^{\beta_{4,y,f,\gamma}}}\right)} - 1}{t2_{\min,y,f,\gamma} - 1} \end{aligned} \tag{A.1.32}$$

where $\beta_{1,y,f,\gamma}$ (P) is the size at which selectivity=1.0 begins for gender γ, $\beta_{2,y,f,\gamma}$ (P) is the size at which selectivity=1.0 ends for gender γ (this is the width of the top, *peak₂* is the endpoint), $\beta_{3,y,f,\gamma}$ (P) determines the slope of the ascending section for gender γ, $\beta_{4,y,f,\gamma}$ (P) determines the slope of the descending section for gender γ, $\beta_{5,y,f,\gamma}$ (P) is the selectivity at $L'_{\min}$ for gender γ, and $\beta_{6,y,f,\gamma}$ (P) is the selectivity at $L'_{\max}$ for gender γ, $t1_{min,y,f,\gamma}$ and $t2_{min,y,f,\gamma}$ are defined as:

$$t1_{\min,y,f,\gamma} = e^{\left(-\frac{\left(L_{\min}-\beta_{1,y,f,\gamma}\right)^2}{e^{\beta_{3,y,f,\gamma}}}\right)} \qquad t2_{\min,y,f,\gamma} = e^{\left(\frac{-\left(L'_{\max}-peak_{2,y,f,\gamma}\right)^2}{e^{\beta_{4,y,f,\gamma}}}\right)} \tag{A.1.33}$$

$peak_{2,y,f,\gamma}$ is the endpoint where selectivity =1.0 for gender γ defined as:

$$peak_{2,y,f,\gamma} = \beta_{1,y,f,\gamma} + L_{\text{width}} + \left(\frac{0.99L'_{\max} - \beta_{1,y,f,\gamma} - L_{\text{width}}}{1+e^{-\beta_{2,y,f,\gamma}}}\right) \tag{A.1.34}$$

L_{width} is the width of each population length bin. The minimum and maximize sizes for the double normal selectivity function can be pre-specified, in which case the ascending and descending limbs are calculated as:

$$asc_{y,f,\gamma,l} = e^{\left(\frac{-\left(L'_l-\beta_{1,y,f,\gamma}\right)}{e^{\beta_{3,y,f,\gamma}}}\right)} \qquad dsc_{y,f,\gamma,l} = e^{\left(\frac{-\left(L'_l-peak_{2,y,f,\gamma}\right)^2}{e^{\beta_{4,y,f,\gamma}}}\right)} \tag{A.1.35}$$

With this approach, the logistic ascending and descending limbs smoothly scale selectivity between the endpoints and the apical value of 1.0.

1.11 Fishery retention

A retention function can be used for each fishery to partition the selected catch into discarded and retained portions. Fisheries are assumed to retain all catch if the retention function is not used. The data for each fishery can be designated as discarded, retained, or combined if retention is modeled. The index *m* for market category is used to designate between these data types. Each retention function is logistic with a specified asymptote (not necessarily 1 as in Equation A.1.36), and a male inflection size can be an arithmetic offset to the female inflection size. Thus four parameters are required. The fraction of the catch in length bin *l*, during year *y*, for fishery *f*, gender γ, and market category *m* is calculated as:

$$b_{y,f,\gamma,l,m} = \begin{cases} 1 & \text{for } m=0 \text{ (combined catch)} \\ 1-\beta_{3,y,f,\gamma,l}\left(1+e^{-\left(L_l-\left(\beta_{1,y,f,\gamma,l}+\beta_{4,y,f,\gamma,l}\right)\right)/\beta_{2,y,f,\gamma,l}}\right)^{-1} & \text{for } m=1 \text{ (discarded catch)} \\ \beta_{3,y,f,\gamma,l}\left(1+e^{-\left(L_l-\left(\beta_{1,y,f,\gamma,l}+\beta_{4,y,f,\gamma,l}\right)\right)/\beta_{2,y,f,\gamma,l}}\right)^{-1} & \text{for } m=2 \text{ (retained catch)} \end{cases} \tag{A.1.36}$$

where $\beta_{1,y,f,\gamma,l}$ (P) is the length at the point of inflection in the retention function, $\beta_{2,y,f,\gamma,l}$ (P) is the parameter determining the slope at the point of inflection, $\beta_{3,y,f,\gamma,l}$ (P) is the asymptotic fraction retained, and $\beta_{4,y,f,\gamma,l}$ (P) is 0 for females and is the offset value for males. In addition, there is an option to provide a discard survival function for situations in which not all the discarded fish die. In this case, the total mortality is the fraction of catch that is retained plus the fraction that is discarded and does not survive.

2. Observation model

The observation model is used to generate expected values for the data while taking into account factors such as selectivity, that influence the relationship between the population and samples from the population, and factors such as ageing error, that influence the relationship between these samples and actual observations. The first step in the observation model is to apply age-length selectivity for a particular fishery/survey to the age-length population at the mid-point of season *t* to calculate the age-length sample from the population. All subsequent expected values for the observations are derived from these age-length samples.

2.1 Survey observation

The catch-at-age and -at-length for time period *t* for survey *f* for length bin *l* and age *a* by gender γ is:

$$C_{t,f,\gamma,a,l} = S_{y,f,\gamma,l} S_{y,f,\gamma,a} \varphi_{t,\gamma,a,l} N_{t,\gamma,a} e^{-timing\left(Z_{t,\gamma,a}\right)} \quad \text{(A.2.1)}$$

where *timing* is the product of the user-specified survey timing and the season duration δ_s. The distribution of lengths at each age is always calculated as if timing = 0.5 although timing is used in the mortality calculation. For surveys that are focused on a particular age of fish, this specificity is reflected in the specified selectivity for that survey.

2.2 Abundance indices

The abundance that is available for observation during time period *t*, for fishery or survey *f* is:

$$B_{t,f} = \sum_{\gamma=1}^{A_\gamma} \sum_{l=1}^{A_l} w_{\gamma,l} \sum_{a=0}^{A} C_{t,f,\gamma,a,l} \quad \text{(A.2.2)}$$

The expected observed abundance by fishery or survey *f* is related to the available population abundance according to:

$$B_{t,f}^{obs} = Q_f B_{t,f} \quad \text{(A.2.3)}$$

where Q_f is the catchability coefficient for the fishery or survey *f*. The weight term is not included in Equation A.2.2 if the survey is in terms of numbers of fish.

The catchability coefficient, Q_f, relates the available population abundance to the expected observed abundance. SS allows for several relationships between the observed and available population abundance through the form of Q_f. The relationships can include non-linearity in survey-abundance linkage, an estimable constant added to the input standard deviation of the survey availability, a simple scaling factor, or as shown in Equation A.2.4 a parameter that creates an environmental effect on $Q_{y,f}$:

$$\log\left(Q_{y,f}\right) = \log\left(Q_{base}\right) + \eta\psi_y \quad \text{(A.2.4)}$$

where Q_{base} (P) is the initial catchability coefficient, η (P) is the *Q*-link parameter, and ψ_y (I) is the value of the environmental data series for year *y*.

2.3 Composition data

Composition data can be in terms of length-, age-, or generalized size-composition, including weight. In each case, a transition matrix is used to convert from the age/length prediction to the units and bin structure of the particular sample.

2.3.1 Length compositions

The expected value for a length-composition observation is created by parsing the age/length predictions from the population length bin structure into the length data bin structure. This is most efficiently done if the boundaries of the data length bins align with the population bins, but the model can interpolate as necessary. However, a data length bin cannot lie entirely within a population length bin. The retention function will be accounted for when calculating the expected size-composition if such as function has been defined. The expected compositions are compressed at the tails to match the degree of tail compression applied to the observed length composition:

$$\hat{p}_{1,y,f,\gamma,l} = \begin{cases} 0 & \text{for } l < l_{1,\gamma} \\ \sum_{l \le l_{1,\gamma}} \hat{p}_{1,y,f,\gamma,l} & \text{for } l = l_{1,\gamma} \\ \hat{p}_{1,y,f,\gamma,l} & \text{for } l_{1,\gamma} < l < l_{2,\gamma} \\ \sum_{l \le l_{2,\gamma}} \hat{p}_{1,y,f,\gamma,l} & \text{for } l = l_{2,\gamma} \\ 0 & \text{for } l > l_{2,\gamma} \end{cases} \qquad \text{(A.2.5)}$$

where $l_{1,\gamma}$ (I) is the accumulator length bin for the lower tail by gender, $l_{2,\gamma}$ (I) is the accumulator length bin for the upper tail by gender, and $\hat{p}_{1,y,f,\gamma,l}$ is the expected proportion of the catch of fish of gender γ in length bin *l* during year *y* (where *t*=*y*) for fishery or survey *f* calculated as:

$$\hat{p}_{1,y,f,\gamma,l} = \frac{\sum_{a=0}^{A} C_{t,f,\gamma,a,l} + x}{\sum_{l=1}^{A_l} \left(\sum_{a=0}^{A} C_{t,f,\gamma,a,l} + x \right)} \qquad \text{(A.2.6)}$$

where *x* (I) is a small constant added to each bin, specified by the user.

2.3.2 Age compositions

Similar to the length-compositions, the expected age-compositions are created from the predicted sample age/length matrix. However, there is a provision to distribute the expected numbers at each true age across a normal distribution of age bins according to a defined aging error matrix with age-composition data. The matrix can incorporate both ageing bias and ageing imprecision and be in terms of age bins that differ in width from true age. Multiple age-transition matrices can be defined, in principal a different matrix for each age sample, but each must use the same age bin structure. The resultant distribution of expected ages is indexed by $\tilde{a}_a$ to designate that these may differ from true age. Here, the expected age value is determined without ageing error, where the proportion at age *a* and gender γ for middle of the year, is calculated as:

$$\Lambda_{\gamma,a} = \begin{cases} \Phi\left(\dfrac{a_1 - \tilde{a}_a}{\tilde{a}_a}\right) & \text{for a} = 1 \\ \Phi\left(\dfrac{a_{a+1} - \tilde{a}_a}{\tilde{a}_a}\right) - \Phi\left(\dfrac{a_a - \tilde{a}_a}{\tilde{a}_a}\right) & \text{for } 1 < a < A \\ 1 - \Phi\left(\dfrac{A - \tilde{a}_a}{\tilde{a}_a}\right) & \text{for } A \end{cases} \tag{A.2.7}$$

where $\tilde{a}_a$ is the expected age *a* incremented to mid-year values by adding 0.5.

The compression of tails of age observations is achieved in a similar fashion as for the length data (Equation A.2.5). The expected proportion of the catch, shown here without ageing error, in each age bin a' for each year *y* for the survey *s* and gender γ is:

$$\hat{p}_{2,y,f,\gamma,a} = \frac{\sum_{l=1}^{A_l} C_{t,f,\gamma,a,l} + x}{\sum_{\gamma=1}^{A_\gamma}\left(\sum_{a=0}^{A} C_{t,f,\gamma,a,l} + x\right)} \tag{A.2.8}$$

3. Statistical Model

The objective function can include contributions from the catch, indices of abundance, discards, observed mean body weights, length-compositions, age-compositions, weight-compositions, mean length-at-age, recruitment, and priors. It is the weighted sum of the individual components indexed by kind of data *i*, and fishery/survey *f* as appropriate:

$$L = \sum_{i=1}^{A_i} \sum_{f=1}^{A_f} \omega_{i,f} L_{i,f} + \omega_R L_R + \sum_{\theta} \omega_\theta L_\theta + \sum_{P} \omega_P L_P \tag{A.3.1}$$

where *L* is the total objective function, *i* is the index for objective function component *i*, A_i (I) is the number of indices, $L_{i,f}$ is the objective function for data kind *i* for fishery or survey *f*, and $\omega_{i,f}$ (I) is a weighting factor for each objective function component. Table A.1 lists the components of the objective function.

3.1 Likelihood Components

The contribution of the indices of abundance to the objective function is:

$$L_{1,f} = \sum_{t=1}^{N_{t,f}} \frac{\left(\ln\left(I_{t,f}\right) - \ln\left(Q_f B_{t,f}\right)\right)^2}{2\sigma^2} + \tilde{\sigma}\ln\left(\sigma_{t,f}\right) \tag{A.3.2}$$

where $N_{t,f}$ (I) is the index for the observed abundance index for time period *t* for by fishery *f*, $I_{t,f}$ (I) is an observed index of abundance for time period *t* and fishery *f* and $\tilde{\sigma}_{t,f}$ (I) is the standard deviation offset value as specified by the user as an additional amount of variance to be added to the CV. Note that a bias correction has been applied in Equation A.3.2, this term can be omitted by the user.

The contribution of the discard to the objective function is based on the assumption of a Student's t-distribution:

$$L_{2,f} = \sum_{f}^{A_f} 0.5\left(df_f + 1\right)\ln\left[\frac{1+\left(d_{y,f} - \hat{d}_{y,f}\right)^2}{df_f \sigma_{y,f}^2}\right] + \tilde{\sigma}\ln\left(\sigma_{y,f}\right) \tag{A.3.3}$$

where d_f (I) is the degrees of freedom, $d_{y,f}$ (I) is the observed discard for year y by fleet f, $\hat{d}_{y,f}$ is the expected discard for year y by fleet f, and $\sigma_{y,f}$ (I) is the standard deviation for discards for year y by fleet f. The contribution of mean body weight to the objective function is also based on the Student's t-distribution:

$$L_{3,f} = \sum_{f}^{A_f} 0.5\left(df_{\bar{w}} + 1\right)\ln\left[\frac{1+\left(\bar{w}_{y,f} - \hat{\bar{w}}_{y,f}\right)^2}{df_{\bar{w}}\left(CV_{\bar{w}}\bar{w}_{y,f}\right)}\right] + \tilde{\sigma}\ln\left(CV_{\bar{w}}\bar{w}_{y,f}\right) \tag{A.3.4}$$

where $df_{\bar{w}}$ (I) is the degrees of freedom for mean body weight, $\bar{w}_{y,f}$ (I) is the observed mean body weight for year y and fishery f, $\hat{\bar{w}}_{y,f}$ is the expected mean body weight for year y and fishery f, and $CV_{\bar{w}}$ (I) is the coefficient of variation for the mean body weight observation.

The contribution of the length-compositions to the objective function is:

$$L_{4,f} = \sum_{y=1}^{N_y}\sum_{\gamma=1}^{A_\gamma}\sum_{l=1}^{A_l} n_{1,y,f,\gamma}\, p_{1,y,f,\gamma,l} \ln\left(p_{1,y,f,\gamma,l} / \hat{p}_{1,y,f,\gamma,l}\right) \tag{A.3.5}$$

where N_y (I) is the index by year, y $n_{1,y,f,\gamma}$ (I) is the specified sample size (indicator of sample precision) for the sample of fish of gender γ for year y for fishery or survey f, $p_{1,y,f,\gamma,l}$ is the observed proportion by year y for fishery or survey f of gender γ which is in length bin l, and $\hat{p}_{1,y,f,\gamma,l}$ is the expected proportion by year y for fishery or survey f of gender γ which is in length bin l (see Equation A.2.6).

Both observed and expected proportions can include a small added constant. The composition sample can also be specified to be joint gender, as above, for females only, for males only, or for combined gender from a two gender population model. An observation can also be treated as combined gender below a specified length and joint gender above that length to take into account difficulties in gender determination for small fish.

The contribution of the age-compositions to the objective function is:

$$L_{5,f} = \sum_{y=1}^{N_y}\sum_{\gamma=1}^{A_\gamma}\sum_{a=1}^{A} n_{2,y,f,\gamma}\, p_{2,y,f,\gamma,a} \ln\left(p_{2,y,f,\gamma,a} / \hat{p}_{2,y,f,\gamma,a}\right) \tag{A.3.6}$$

where $n_{2,y.f,\gamma}$ is the specified sample size for the sample of fish of gender γ for year y for fishery or survey f, $p_{2,y,f,\gamma,a}$ is the observed proportion of the sample during year y for fishery or survey f of gender γ which is of age a, and $\hat{p}_{2,y,f,\gamma,a}$ is the expected proportion during year y for fishery or survey f of gender γ which is age a (see Equation A.2.8).

The contribution of generalized size frequency to the negative of the log-likelihood function is:

$$L_{6,f} = \sum_{y=1}^{N_y}\sum_{\gamma=1}^{A_\gamma}\sum_{l=1}^{A_l} n_{3,y,f,\gamma}\, p_{3,y,f,\gamma,l} \ln\left(p_{3,y,f,\gamma,l} / \hat{p}_{3,y,f,\gamma,l}\right) \tag{A.3.7}$$

where $n_{3,y,f,\gamma}$ (I) is the effective sample size for the sample of fish of gender γ for year *y* for fishery or survey *f*, $p_{3,y,f,\gamma,l}$ is the observed proportion by size and gender in the sample during year *y* for fishery or survey *f*, and $\hat{p}_{3,t,f,\gamma,l}$ is the expected proportion by size in the sample during year *y* for fishery or survey *f*.

The contribution of the catch for each time period *t* to the objective function is:

$$L_{7,f} = \sum_{t=1}^{N_t} \frac{\left(\ln\left(C_{t,f}\right) - \ln\left(\hat{C}_{t,f} + x\right)\right)^2}{2\sigma_{t,f}^2} \tag{A.3.8}$$

where N_t (I) is the index by time *t*, and *x* is a small added constant (1.0E-6). Time periods with zero catches are excluded from the likelihood calculation.

The contribution of the initial equilibrium catch to the objective function is:

$$L_{7,f} = \sum_{f=1}^{A_f} \frac{\left(\ln\left(C_{0,f}\right) - \ln\left(\hat{C}_{0,f} + x\right)\right)^2}{2\sigma_{0,f}{}^2} \tag{A.3.9}$$

The contribution of the *F* ballpark value to the objective function is:

$$\begin{aligned} L' &= e^{\left|\ln\left(F_b/F_y\right)\right|} - 1 \\ L_F &= \frac{xL'}{x + L'} \end{aligned} \tag{A.3.10}$$

where F_b (I) is the ballpark *F* value for user-specified year *y*, F_y is the estimated *F* value for year *y*, and *x* is a scaling constant (1.0E4).

3.2 Recruitment deviations

The contribution of the deviations in recruitment to the objective function is:

$$L_R = \frac{1}{2}\left[\sum_{y=1}^{N_y} \frac{\tilde{R}_y^2}{\sigma_R^2} + b_y \ln\left(\sigma_R^2\right)\right] \tag{A.3.11}$$

The second term of the recruitment deviation penalty scales according to the recruitment bias adjustment parameter which can range from 1.0 for data-rich, to 0.0 for data-poor years.

3.3 Parameter priors

Normal, lognormal, beta, and symmetric beta distributions can be used to create priors for estimated parameters. ADMB requires bounds on all parameters and SS allows the user to define parameter bounds regardless of the assumed distribution.

The normal prior distribution for a parameter θ has the form:

$$L_\theta = 0.5\left(\frac{\theta - \mu_\theta}{\sigma_\theta}\right)^2 \tag{A.3.12}$$

where θ is the parameter, μ_θ (I) is the prior mean value of the parameter, and σ_θ (I) is the standard deviation for the parameter's prior.

The contribution to the objective function for the symmetric beta priors is given by:

$$L_\theta = -\sigma_\theta \Big(\big(\ln\big(0.5(\theta_{\max}+\theta_{\min})-\theta_{\min}\big)+\ln(0.5) \big) + \ln\big(\theta-\theta_{\min}+0.0001\big) + \ln\Big(1-\big(\theta-\theta_{\min}-0.0001\big)/\big(\theta_{\max}-\theta_{\min}\big)\Big) \Big) \tag{A.3.13}$$

where $\theta_{\min}$ (I) is the lower bound for the parameter prior, $\theta_{\max}$ (I) is the upper bound for the parameter prior, and σ_θ (I) is a scalar for the degree of variance.

The contribution to the objective function for the full beta priors is given by:

$$\begin{aligned} L_\theta = &\left(1-\theta_\beta\right)\ln\left(0.0001+\theta-\theta_{\min}\right)+\left(1-\theta_\alpha\right)\ln\left(0.0001+\theta_{\max}-\theta\right)- \\ &\left(1-\theta_\beta\right)\ln\left(0.0001+u_\theta-\theta_{\min}\right)-\left(1-\theta_\alpha\right)\ln\left(0.0001+\theta_{\max}-u_\theta\right) \end{aligned} \tag{A.3.14}$$

where $\theta_{\min}$ (I) is the lower bound for the parameter prior, $\theta_{\max}$ (I) is the upper bound for the parameter prior, $\mu' = \left(\mu_\theta-\theta_{\min}\right)/\left(\theta_{\max}-\theta_{\min}\right)$ is the prior rescaled into [0,1], $\tau = \left(\mu_\theta-\theta_{\min}\right)\left(\theta_{\max}-\mu_\theta\right)/\sigma_\theta^2-1$ is an intermediate quantity, $\theta_\alpha = \tau\left(1-\mu'\right)$ is a derived quantity, and $\theta_\beta = \tau\mu'$ is a derived quantity.

The lognormal prior distribution for a parameter θ has the form:

$$L_\theta = 0.5\left(\frac{\ln(\theta)-\mu_\theta}{\sigma_\theta}\right)^2 \tag{A.3.15}$$

3.4 Parameter deviations

When parameters for natural mortality, growth and selectivity are allowed to vary as random deviations over time, the contribution to the objective function for deviations in these parameters to the objective function is:

$$L_P = \frac{1}{2\sigma_P^2}\sum\nolimits_{y=1}^{N_y}\tilde{P}_y^2 \tag{A.3.16}$$

where σ_P (I) is the user-input standard deviation of the process and $\tilde{P}_y^2$ is the exponential deviation of the parameter P for year y.

3.5 Crash penalties

In addition to the objective function components above, there is a penalty function whenever the harvest rate for a particular fishery is above a user-specified value, typically 0.9 for Pope's approximation. This penalty function also traps for negative abundance of a particular age occurring due to the cumulative removals from several fisheries.

4. Management quantities

A powerful aspect of integrated analysis models is the ease with which they can transition from estimation of the historical and current population sizes, to simulation of forecasted population sizes. The forecast depends upon some particular level of fishing mortality, which typically is based on rates that would achieve *MSY* or a proxy for *MSY*. The quantities related to target and limit fishing mortality rates are commonly referred to as reference points because they establish the threshold for overfishing determinations. Alternatively, a pre-specified catch level can also be applied during forecast.

Reference points and forecasts depend on the pattern of fishery selectivity and the relative intensity of fishing between fleets that have different selectivity patterns. The calculation starts by using user-inputs to create the time-averaged selectivity for each fleet, the relative fishing intensity between fleets, and the time-averaged biology (body weight-at-age) to use in the reference point calculations. Similarly, there are inputs for forecast, except the forecast biology is based on growth of extant cohorts at the end of the estimation time series. Next, the fishing intensity multiplier (applied across all fleets according to their relative fishing intensity) that would achieve, in equilibrium, a specified level of spawning biomass-per-recruit (*SPR*) relative to the unfished level of spawning biomass-per-recruit is found. The multiplier that would achieve a specified level of absolute spawning biomass (B_{tgt}) relative to the unfished spawning biomass while taking the spawner-recruitment relationship into account is then found. Finally, the multiplier that would produce the largest yield (*MSY*) also while taking the spawner-recruitment relationship into account is found. These and various associated quantities are reported along with the estimates of variance. The forecast which uses either the *F* associated with *SPR*, B_{tgt}, *MSY* or some other user specification to forecast stock abundance and catch into the future is then conducted. The forecast module includes annual forecast recruitment deviations as estimated quantities, and can include annual catch implementation error as an estimated quantity to account for a realistic degree of variability in the derived forecast quantities. The forecast also proceeds through three stages to provide for forecasts using *F* limits and then *F* targets to provide information on the probability that harvesting according to the *F* target would exceed the F_{lim} or that the stock would decline below some biomass.

4.1 Reference Points

The calculation of reference points is built upon a dynamic pool approach that first calculates the equilibrium spawning biomass-per-recruit that would occur for a specified input level of fishing intensity (with associated fishery selectivity and relative fishing intensity between fleets). These equilibrium quantities are then used with the spawner-recruitment function to calculate absolute equilibrium levels of spawning biomass, recruitment and yield for the specified level of fishing intensity. For example, the equilibrium spawning biomass and recruitment are as follows for the Beverton-Holt spawner-recruitment curve:

$$SB_{tgt} = \frac{4hR_0 SB_{equil} - S_0\left(1-h\right)}{5h-1} \qquad R_{tgt} = \frac{4hR_0 S_{tgt}}{S_0\left(1-h\right)+S_{tgt}\left(5h-1\right)} \qquad \text{(A.4.1)}$$

where SB_{equil} is the spawning biomass-per-recruit in equilibrium conditions for a selected harvest policy.

SS provides three reference points: the first is calculated by finding the *F* multiplier that would achieve a specified level of spawning biomass-per-recruit relative to the unfished level of spawning biomass-per-recruit; the second searches for the *F* multiplier that would achieve a specified level of spawning biomass relative to the unfished level of spawning biomass while taking the spawner-recruitment relationship into account; and the third searches for the *F* multiplier that would produce the maximum equilibrium yield, also taking the spawner-recruitment relationship into account. Each of these levels is calculated by an iterative search over a specified number of steps. SS output quantities, with variance, for each include: *F*, biomass, catch and recruitment.

4.2 Forecast

The forecast module provides the capability to conduct a projection for a user-specified number of years that is directly linked to the model's ending conditions, associated uncertainty, and to a specified level of fishing intensity. The forecast module applies a multiple pass approach to calculate both the Overfishing Limit (OFL; a level of harvest that if exceeded would constitute overfishing) and the Acceptable Biological Catch (ABC; a level of harvest that accounts for scientific uncertainty in the estimate of the OFL, and is less or equal to the OFL) in a single model run. More importantly, the multiple passes mimic the actual sequence of assessment-management action over a multi-year period for many fisheries (see Table A.2 for outline of sequence of calculations). The first pass calculates the OFL based on catching the OFL each year, and represents the absolute maximum upper limit to catches. The second pass forecasts a catch based on a harvest policy, then applies catch caps and allocations, then updates the *F*'s to match these catches. In the third pass, stochastic recruitment and catch implementation error are evoked and the *F* that would be needed to catch the adjusted catch amount previously calculated in the second pass is calculated. It is possible to use this approach to produce improved estimates of the probability that *F* would exceed the overfishing *F*.

The first pass of the forecast module determines the benchmark quantities based upon spawning biomass and the resulting recruitment in the absence of deviations. The resulting catch from F_{lim}, the OFL, dependent upon the age-structure of the population is removed. Implementation error is ignored in this first pass, along with any fixed input catches with no catch adjustments for caps and allocations. For each forecast year, the OFL is conditioned on catching the OFL each year during this first pass.

The second pass of the forecast module consists of three steps to calculate both an OFL and an ABC, assuming that the ABC is caught each year. The first step in the first forecast year calculates the OFL ignoring input catches, caps and allocations, and implementation error, similar to the method applied in the first pass. The second step predicts the ABC that would result from F_{tgt} (adjustment to the F_{lim} based upon a control rule depending upon current stock status). If a fixed input catch is specified for the current forecast year, that value then replaces the calculated ABC, after which any catch adjustments (caps and allocations) are applied on an annual basis (after looping through seasons and areas within this year). At this stage no implementation error is applied to the catch. The last step determines the *F* that would result based on any of the adjustments to the catch, which then determines the survivors to pass into the next forecast year accordingly.

The third and final pass of the forecast module begins by determining the spawning biomass and resulting recruitment with recruitment deviations. The catches calculated during the second pass of the forecast are multiplied by random implementation error, then used to calculate the *F* that would result from catching this adjusted catch from a population which is now fluctuating due to the random recruitment deviations. Thus, the estimates of variance in forecast spawning biomass and *F* take into account both recruitment variability, implementation error, and lack of knowledge of recruitment deviations when the ABC is calculated.

4.2.1 U.S. west coast groundfish control rule

The adjustment to *F* based upon the West Coast groundfish control rule (PFMC, 2011) is composed of three sections; relative spawning biomass less than the minimum relative spawning biomass level, relative spawning biomass between the minimum and the target relative spawning biomass level, and relative spawning biomass larger than the target relative spawning biomass level. The three parts and the subsequent applied ABC_{buffer} and adjusted F are:

$$
\begin{aligned}
&Left = \left(0.0001\frac{SB_y}{\left(H_{\lim}SB_0\right)}\right)j_1 \\
&Curve = \left(0.0001+\left(1-0.0001\right)\left(\frac{H_{tgt}SB_0}{SB_y}\right)\left(\frac{SB_y-H_{\lim}SB_0}{H_{tgt}SB_0-H_{\lim}SB_0}\right)\right)\left(1-j_1\right) \\
&Right = 1-j_2 \\
&ABC_{buffer} = H_s\left(j_2\left(Left+Curve\right)+H_s\left(Right\right)\right) \\
&F_{adj} = F_{tgt}ABC_{buffer}
\end{aligned}
\tag{A.4.2}
$$

where H_{lim} (I) is the minimum relative spawning biomass level, H_{tgt} (I) is the target relative spawning biomass level, and H_s (I) is the scale of the harvest. Adjustments to catch apply the logistic joiner approach so the overall results remain completely differentiable as:

$$
\begin{aligned}
j_1 &= \left(1-\mathrm{e}^{10\left(SB_y-H_{tgt}SB_0\right)}\right)^{-1} \\
j_2 &= \left(1-e^{10\left(SB_y-H_{\lim}SB_0\right)}\right)^{-1}
\end{aligned}
\tag{A.4.3}
$$

4.2.2 U.S. Alaska harvest policy

$$
\begin{aligned}
&Left = \left(0.0001\frac{SB_y}{\left(H_{\lim}SB_0\right)}\right)j_1 \\
&Curve = \left(0.0001+\left(1-0.0001\right)\frac{\left(SB_y-H_{\lim}SB_0\right)}{\left(H_{tgt}SB_0-H_{\lim}SB_0\right)}\right)\left(1-j_1\right) \\
&Right = 1-j_2 \\
&ABC_{buffer} = H_s\left(j_2\left(Left+Curve\right)+H_s\left(Right\right)\right) \\
&F_{adj} = F_{tgt}ABC_{buffer}
\end{aligned}
\tag{A.4.4}
$$

5. Advanced options

5.1 Natural mortality

Lorenzen (1996) natural mortality is based on the concept that natural mortality varies over the life cycle of a fish, which is driven by physiological and ecological processes. The Lorenzen natural mortality rate is calculated as a function of the size of fish relative to the size at a specified reference age:

$$M_{\gamma,a} = \begin{cases} M_{\gamma,0} & \text{if } a = 0 \\ \ln\left(L_{t,\gamma,a} \big/ \left(r_1 + L_{t,\gamma,a}\right)\right) r_2 & \text{if } a > 0 \end{cases} \tag{A.5.1}$$

$$r_1 = L_{\infty,\gamma} \exp^{-k_\gamma \cdot \sum_{s=1}^{A_s} \delta_s} - 1 \quad r_2 = \frac{\alpha_\gamma}{\ln\left(L_{t,\gamma,a} \big/ \left(r_1 + L_{t,\gamma,a}\right)\right)}$$

where r_1 and r_2 determine the rate of change for natural mortality by age, and α_γ (I) is the parameter for each gender that will scale *M* at the reference age.

5.2 Alternative maturity and fecundity options

Maturity-at-age:

$$Mat_a = \left(1 + e^{\Omega_4 (a - \Omega_3)}\right) \tag{A.5.2}$$

Eggs as a function of length and weight:

$$Eggs_l = \Omega_5 \left(L_l'\right)^{\Omega_6} \quad Eggs_l = \Omega_5 \left(w_{\text{fem},l}\right)^{\Omega_6} \quad Eggs_l = \Omega_5 + L_l' \Omega_6 \tag{A.5.3}$$

5.3 Recruitment Options

5.3.1 Ricker

$$R_t = \left(\frac{R_0 SB_y}{SB_0}\right) e^{h\left(1 - SB_y / SB_0\right)} e^{-0.5 b_y \sigma_R^2 + \tilde{R}_y} \quad \tilde{R}_y \sim \tilde{N}\left(0; \sigma_R^2\right) \tag{A.5.4}$$

5.3.2 Survival-based

Survival-based recruitment (Taylor et al., this volume) is constrained so that the recruitment rate cannot exceed fecundity

$$R_t = e^{\left(-z_0 + \left(z_0 - z_{\min}\right)\left(1 - \left(SB_y / SB_0\right)^{\rho}\right)\right)} SB_y e^{-0.5 b_y \sigma_R^2 + \tilde{R}_y} \quad \tilde{R}_y \sim \tilde{N}\left(0; \sigma_R^2\right) \tag{A.5.5}$$

where z_0 (P) is the negative log of the pre-recruit mortality rate at unfished equilibrium, z_{min} is the limit of the pre-recruit mortality as relative spawning biomass approaches zero, parameterized as a function of z_{frac} (P) (which represents the reduction in mortality as a fraction of z_0), and ρ (P) is a parameter controlling the shape of density-dependent relationship between relative spawning biomass and pre-recruit survival. The steepness (*h*) of the spawner-recruit curve (defined as recruitment relative to R_0 at a spawning depletion level of 0.2) is:

$$h = 0.2 e^{z_0 z_{frac}\left(1 - 0.2^{\beta}\right)} \tag{A.5.6}$$

5.3.3 Hockey-Stick

The hockey-stick recruitment curve is calculated as:

$$R_t = R_{\min} R_0 + \left(\frac{SB_y}{hSB_0}\right)\left(R_0 - R_{\min}\right)\left(join\right) + R_0\left(1 - join\right)$$

$$join = \left[1 + e^{\left(1000*\left(SB_y - hSB_0\right)\big/ SB_0\right)}\right]^{-1} \tag{A.5.7}$$

where $R_{\min}$ (I) is the pre-specified minimum recruitment level predicted at a spawning size of zero, and h (I) is the fraction of SB_0 below which recruitment declines linearly.

5.4 Movement

The movement between areas p is calculated by assuming that movement either increases or decreases linearly (in log-space) with age a:

$$X_{s,p',p,a} = \begin{cases} \dfrac{\left(1-\lambda^p\right)e^{x_{s,p',p,a}}}{1+e^{x_{s,p',p,a}}} & \text{if } p' = p'' \\ \dfrac{\lambda^p e^{x_{s,p',p,a}}}{1+e^{x_{s,p',p,a}}} & \text{otherwise} \end{cases} \tag{A.5.8}$$

$$x_{s,p',p,a} = \begin{cases} m_{\alpha,s,p',p} & a \le a_\alpha \\ m_{\alpha,s,p',p} + \left(a - a_\alpha\right)\left(\dfrac{m_{\omega,s,p',p} - m_{\alpha,s,p',p}}{a_\alpha - a_\omega}\right) & a_\alpha < a < a_\alpha \\ m_{\omega,s,p',p} & a \ge a_\omega \end{cases} \tag{A.5.9}$$

where $m_{\alpha,s,p',p}$ (P) is the probability (in log space) of moving from area *p'* to area *p* for age a_α (I), the age where fish start movement, and $m_{\omega,p',p}$ (P) is the probability (in log space) of moving from area *p'* to area *p* for age a_ω (I), the age where fish end movement.

5.5 Tag recapture data

SS allows for the integration of tag-recapture data to estimate movement rates and abundance. Each tag group is modeled using the same mortality, selectivity, and movement equations used for the total population, except that recruitment to the tagged population occurs through releases, and can therefore occur at any age. Tag-groups experience natural and fishing mortality, in common with untagged fish, but can also experience an additional tag-related mortality. Tagged fish released into areas are assumed to distribute randomly among fish of the same age in the release area. Release groups are uniquely identified and are modeled as a separate entity. Numbers of tagged fish are assumed negligible relative to non-tagged fish, so total mortality of all fish is not affected by tag-induced mortality.

The implementation of tag-recapture relies upon a major simplification relative to implementations in CASAL (Bull et al., 2005) and MULTIFAN-CL (Fournier et al., 1998). In other implementations, tag groups have an initial size distribution which is spread across a range of ages according to the growth model. This spread would be according to the dynamics if growth parameters were being estimated. In SS, the simplification requires users to assign an age-at-release so that all the tagged fish of that group are from a single cohort. If tagging was actually applied to a wide size range, then breaking the releases into two or more tag groups with different assigned ages at tagging is appropriate.

SS first calculates the number released by platoon by distributing total releases according to the proportion of population numbers by platoon at age-of-release in the release area calculated as:

$$T_{\kappa,p,g,0} = N_{\kappa} \frac{N_{t,p,g,a}}{\sum_{g=1}^{A_g} N_{t,p,g,a}} \tag{A.5.10}$$

where N_{κ} is the number of released fish by tag group κ, $N_{t,p,g,a}$ is the population number of fish at the start of time period *t* in area *p* of platoon *g* at age *a*, and A_g (I) in the number of platoons. The number released by platoon (Eqn. A.5.10) can be either calculated as a combined-gender release group or a gender-specific release group. Initial tag loss is then applied by tag group to the tagged population as:

$$T_{\kappa,p,g,0} = T_{\kappa,p,g,0}\left(1-\varpi_i\right) \tag{A.5.11}$$

where ϖ_i is the initial tag-loss.

Expected tag-recapture rates are estimated based on releases for a specified age in a specified area at a specified time and recaptures by fleets. Fleets in SS operate in only a single area, so recaptures contain information on movement. The expected tag-recaptures from a tag group by fishery and season since tag release is modeled by the continuous *F* calculated as:

$$\hat{R}_{\kappa,\delta_t f} = \sum\nolimits_g^{A_g} \sum\nolimits_p^{A_p} T_{\kappa,p,g,\delta_t} \left(1-e^{-\delta_s\left(Z_{y,p,a1}+\varpi_c\right)}\right) \frac{S_{y,f,a1}F_{y,f}}{Z_{y,p,a1}+\varpi_c} \left(r_f e^{\delta_t \Delta_f}\right) \tag{A.5.12}$$

where A_p (I) is the number of areas, κ is the tag group, $S_{y,f,a1}$ (P) is the selectivity for fishery *f* for fish at the age of release *a1* (I), $Z_{p,a1}$ (P) is the total mortality for area *p* for fish at the age of release *a1*, ϖ_c (P) is the chronic tag-loss or mortality rate, r_f (I) is the tag recapture reporting rate for fishery *f*, δ_t is the time counter (in seasons) for tag groups, and Δ_f (P) is the tag-recapture reporting decay rate which is approximated with an asymptotic curve related to the number of tag groups and fleets.

The surviving tagged fish by tag group κ in area *p* available for recapture using the next period, $T_{\kappa,p,g,\delta_{t+1}}$, is updated as:

$$T_{\kappa,p,g,\delta_{t+1}} = T_{\kappa,p,g,\delta_t} e^{-\delta_s\left(Z_{t,p,g,a1}+\varpi_c\right)} \tag{A.5.13}$$

Alternatively, if the Pope's approximation for fishing mortality is applied, the expected tag-recapture by tag group is calculated as:

$$\hat{R}_{\kappa,\delta_t,f} = \sum\nolimits_g^{A_g} \sum\nolimits_p^{A_p} T_{\kappa,p,g,\delta_t} e^{-\delta_s\left(M_{s,g,a1}+\varpi_c\right)} S_{y,g,f,a1} F_{t,f} r_f e^{\delta_t \Delta_f} \tag{A.5.14}$$

and

$$T_{\kappa,p,g,\delta_{t+1}} = T_{\kappa,p,g,\delta_t}\left(N_{t+1,p,g,a1}+x\right)\Big/\left(N_{t,p,g,a1-1}+x\right)\left(1-\delta_s\varpi_c\right) \tag{A.5.15}$$

where x is a small added constant (1.0e-10).

Tagged fish are allowed to move between areas according to movement rates by age (eqns. A.5.8 and A.5.9). Also, similar in concept, if a population is hermaphroditic, tagged fish are allowed to change from one sex to the other and are tracked accordingly in the number of tagged fish available for recapture.

The likelihood contribution for the tag-recapture data is separated into two parts; one for the distribution of recaptures among fleets to help estimate movement between areas, and the other based on the temporal sequence of recaptures summed across all fleets to help estimate overall mortality rates. The multinomial likelihood for distribution across fleets for the time following an initial mixing period is calculated as:

$$\begin{aligned} p_{4,\kappa,\delta_t,f} &= \frac{\hat{R}_{\kappa,\delta_t,f}+x}{\sum_{f=1}^{A_f}\hat{R}_{\kappa,\delta_t,f}+x} \\ L_{6,\kappa} &= \sum_{\delta_t=mixing}^{T\max} R_{\kappa,\delta_t}\sum_{f=1}^{A_f} R'_{\kappa,\delta_t,f}\ln\left(p_{4,\kappa,\delta_t,f}\right) \end{aligned} \tag{A.5.16}$$

where x is a small added constant (1.0e-6), $\hat{R}_{\kappa,\delta_t,f}$ is the expected proportion by fleet, R_{κ,δ_t} is the total observed recaptures for the for the time period, *mixing* (I) is a latency period for tagged fish to mix into the population, and $R'_{\kappa,\delta_t,f}$ is the observed proportion of these recaptures by fleet. The second part of the tag-recapture likelihood, the recaptures over time, is calculated according to the log transformed negative binomial distribution based on the expected total recaptures across all areas and the observed recaptures:

$$\begin{aligned} L_{7,f} = {} & \ln\left(\Gamma\left(\hat{R}_{\kappa,\delta_t,f}+o\right)\right)-\ln\left(\Gamma(o)\right)-\ln\left(\hat{R}_{\kappa,\delta_t,f}!\right)+o\ln(o)+ \\ & \hat{R}_{\kappa,\delta_t,f}\ln\left(R_{\kappa,\delta_t,f}\right)-\left(o+\hat{R}_{\kappa,\delta_t,f}\right)\ln\left(o+R_{\kappa,\delta_t,f}\right) \end{aligned} \tag{A.5.17}$$

where o is a derived parameter calculated as:

$$o = \hat{R}_{\kappa,\delta_t,f}\Big/\left(10^{-120}+O_p-1\right) \tag{A.5.18}$$

where O_p (I) is the over-dispersion input parameter.

5.6 Fishing Mortality

5.6.1 Pope's Approximation

The exploitation rate for time period t for time period t for fishery f is:

$$F_{t,f} = C^{obs}_{t,f,retained} \,/\, B_{t,f} \tag{A.5.19}$$

where $B_{t,f}$ is the total vulnerable, retainable biomass at the start of time period t for fishery f.

Although the harvest rate calculation is based on the retained catch, the resultant mortality must take total catch into account. The harvest rate F calculated from retained catch is applied to the total available numbers to calculate the expected number in the total catch for time-step *t* for fishery *f* as:

$$C_{t,f,\gamma,a} = F_{t,f} \sum_{l=1}^{A_l} \phi_{\gamma,a,l} \, S_{t,y,f,\gamma,l} \left(N_{t,\gamma,a} e^{-\delta_s M_{\gamma,a}} \right) \tag{A.5.20}$$

This estimated catch is removed from the population is:

$$N_{t+1,\gamma,a} = \left(N_{t,\gamma,a-s_0} - \sum_{f=1}^{A_f} \sum_{l=1}^{A_l} C_{t,f,\gamma,a-s_0,l} \right) e^{-0.5\delta_0 M_{\gamma,a}} \tag{A.5.21}$$

where s_0 is an indicator of the first season. It accounts for the convention that fish progress to the next age on Jan 1 and is calculated as:

$$s_0 = \begin{cases} 1 & \text{if } s = 1, \\ 0 & \text{else,} \end{cases} \tag{A.5.22}$$

Note that removals are summed across lengths for each platoon, morph, and age. The retained catch computations above are identical to total catch calculations when a retention function is not used, or is set to retain all fish. The nature of the harvest rate calculation creates the possibility that the catch could be greater than the available biomass during some model iterations while it is searching for the best parameter combination. The possibility of negative abundance is even greater for individual ages when there are multiple fisheries. A penalty function is necessary to keep the model from crashing when it temporarily encounters these negative abundance situations. This penalty is described in Section 3.5.

5.6.2 Continuous F Method

The catch for time period *t*, of gender γ of age *a* fish is calculated equation A.1.23.

5.7 Catch-at-length

The catch-at-length *l* is not used in the mortality calculations directly, but it is a useful output quantity and an intermediate for calculation of survey biomass. It is calculated as:

$$\begin{aligned} \lambda_{t,\gamma,a} &= 1 - \exp^{\left(-\delta_{s,f} Z_{t,\gamma,a}\right)} \\ C_{t,f,\gamma,l} &= \sum_{a=0}^{A} \varphi_{t,\gamma,a,l} S_{y,f,\gamma,l} N_{t,\gamma,a} \lambda_{t,\gamma,a} \end{aligned} \tag{A.5.23}$$

where $Z_{t,\gamma,a}$ is total mortality (Equation A.1.21). The catch in weight for time period *t* by fleet *f* is calculated as:

$$C_{t,f} = \sum_{\gamma=1}^{A_\gamma} \sum_{l=1}^{A_l} w_{\gamma,l} C_{t,f,\gamma,l} \tag{A.5.24}$$

5.8 Selectivities

5.8.1 Double Logistic

$$\begin{aligned} S_{y,f,\gamma,l} = & \left(\left(asc_{y,f,\gamma,l} \, j_{1,y,f,\gamma,l} \right) + \left(1 - j_{1,y,f,\gamma,l} \right) \right) j_{2,y,f,\gamma,l} + \\ & dsc_{y,f,\gamma,l} \left(1 - j_{2,y,f,\gamma,l} \right) j_{3,y,f,\gamma,l} + final_{y,f,\gamma,l} \left(1 - j_{3,y,f,\gamma,l} \right) \end{aligned} \tag{A.5.25}$$

where the joiner functions, ascending and descending components are:

$$j_{1,y,f,\gamma,l}=\left(1+e^{10\left(L'_l+\beta_{1,y,f,\gamma}\right)}\right)^{-1}$$

$$j_{2,y,f,\gamma,l}=\left(1+e^{10\left(L'_l-\left(\beta_{1,y,f,\gamma}+\beta_{8,y,f,\gamma}\right)\right)}\right)^{-1}$$

$$j_{3,y,f,\gamma,l}=\left(1+e^{10\left(L'_l-L'_{\max}\right)}\right)^{-1}$$

$$asc_{y,f,\gamma,l}=\beta_{2,y,f,\gamma}+\left(1-\beta_{2,y,f,\gamma}\right)\left(\frac{\left(1+e^{-e^{\beta_{4,y,f,\gamma}}\left(L'_l-t_{1,y,f,\gamma}\right)}\right)^{-1}-t_{1,y,f,\gamma,\min}}{t_{1,y,f,\gamma,\max}-t_{1,y,f,\gamma,\min}}\right)^{t_{1,y,f,\gamma,\text{power}}}$$

$$dsc_{y,f,\gamma,l}=\left(1+\left(\left(1+e^{-\beta_{5,y,f,\gamma}}\right)^{-1}-1\right)\right)\left|\left(\frac{\left(1+e^{-e^{\beta_{7,y,f,\gamma}}\left(L'_l-t_{2,y,f,\gamma}\right)}\right)^{-1}-t_{2,y,f,\gamma,\min}}{t_{2,y,f,\gamma,\max}-t_{2,y,f,\gamma,\min}}\right)^{t_{2,y,f,\gamma,\text{power}}}\right| \tag{A.5.26}$$

where $\beta_{1,y,f,\gamma}$ (P) is the size at which selectivity=1.0 ends for gender γ, $\beta_{2,y,f,\gamma}$ (P) is the size at which selectivity=1.0 begins for gender γ, $\beta_{3,y,f,\gamma}$ (P) is the size at which selectivity is halfway between $\beta_{2,y,f,\gamma}$ (initial) and selectivity = 1.0 for gender γ, $\beta_{4,y,f,\gamma}$ (P) determines the slope of the ascending section for gender γ, $\beta_{5,y,f,\gamma}$ (P) is the selectivity at $L'_{\max}$ for gender γ, $\beta_{6,y,f,\gamma}$ (P) is the size at which the right side of the selectivity is halfway between $\beta_{1,y,f,\gamma}$ (peak) + $\beta_{8,y,f,\gamma}$ (peak width) and $L_{\max}$ for gender γ, $\beta_{7,y,f,\gamma}$ (P) determines the slope of the descending section for gender γ, $\beta_{8,y,f,\gamma}$ (P) is the width of the flattop at peak selectivity for gender γ, $t_{1,y,f,\gamma}$ is defined as:

$$t_{1,y,f,\gamma}=L_{\min}+\left(\beta_{1,y,f,\gamma}-L_{\min}\right)\left(1+e^{-\beta_{3,y,f,\gamma}}\right)^{-1} \tag{A.5.27}$$

$t_{1,y,f,\gamma,\min}$ and $t_{1,y,f,\gamma,\max}$ are defined as:

$$t_{1,y,f,\gamma,\min}=0.9999\left(1+e^{-e^{\beta_{4,y,f,\gamma}}\left(L'_{\min}-t_{1,y,f,\gamma}\right)}\right)^{-1}$$

$$t_{1,y,f,\gamma,\max}=1.0001\left(1+e^{-e^{\beta_{4,y,f,\gamma}}\left(\beta_{1,y,f,\gamma}-t_{1,y,f,\gamma}\right)}\right)^{-1} \tag{A.5.28}$$

$t_{1,y,f,\gamma,\text{power}}$ is defined as:

$$t_{1,y,f,\gamma,\text{power}}=\frac{\ln(0.5)}{\ln\left(\left(0.5-t_{1,y,f,\gamma,\min}\right)/\left(t_{1,y,f,\gamma,\max}-t_{1,y,f,\gamma,\min}\right)\right)} \tag{A.5.29}$$

$t_{2,y,f,\gamma}$ is defined as:

$$t_{2,y,f,\gamma} = \left(\beta_{1,y,f,\gamma} + \beta_{8,y,f,\gamma}\right) + \left(L_{\max} - \left(\beta_{1,y,f,\gamma} + \beta_{8,y,f,\gamma}\right)\right)\left(1 + e^{-\beta_{6,y,f,\gamma}}\right)^{-1} \tag{A.5.30}$$

$t_{2,t,f,\gamma,\min}$ and $t_{2,t,f,\gamma,\max}$ are defined as:

$$\begin{aligned} t_{2,y,f,\gamma,\min} &= 0.9999\left(1 + e^{-e^{\beta_{7,y,f,\gamma}}\left(\beta_{1,y,f,\gamma} + \beta_{8,y,f,\gamma} - t_{2,y,f,\gamma}\right)}\right)^{-1} \\ t_{2,y,f,\gamma,\max} &= 1.0001\left(1 + e^{-e^{\beta_{7,y,f,\gamma}}\left(L'_{\max} - t_{2,y,f,\gamma}\right)}\right)^{-1} \end{aligned} \tag{A.5.31}$$

$t_{2,t,f,\gamma,\text{power}}$ is defined as:

$$t_{2,y,f,\gamma,\text{power}} = \frac{\ln(0.5)}{\ln\left(\left(0.5 - t_{2,y,f,\gamma,\min}\right) / \left(t_{2,y,f,\gamma,\max} - t_{2,y,f,\gamma,\min}\right)\right)} \tag{A.5.32}$$

5.8.2 Exponential-logistic

$$S_{y,f,\gamma,l} = \frac{e^{\beta_{3,y,f,\gamma}\beta_{1,y,f,\gamma}\left(peak_{y,f,\gamma} - L'_l\right)}}{1 - \beta_{3,y,f,\gamma}\left(1 - e^{\beta_{1,y,f,\gamma}\left(peak_{y,f,\gamma} - L'_l\right)}\right)} \tag{A.5.33}$$

where $\beta_{1,y,f,\gamma}$ (P) is the size at which selectivity=1.0 begins for gender γ, $\beta_{3,y,f,\gamma}$ (P) determines the slope of the ascending section for gender γ, $peak_{y,f,\gamma}$ is the peak of selectivity calculated as:

$$peak_{y,f,\gamma} = L'_{\min} + \beta_{2,y,f,\gamma}\left(L'_{\max} - L'_{\min}\right) \tag{A.5.34}$$

where $\beta_{2,y,f,\gamma}$ (P) is the size at which selectivity=1.0 ends for gender γ (this is the width of the top, $peak_{y,f,\gamma}$ is the endpoint).

References

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Pacific Fishery Management Council, (PFMC). 2011. Pacific Coast Groundfish Fishery Management Plan. Pacific Fishery Management Council, Portland, OR, 146 pp.

Tables

Table A.1 Components of the objective function

index	Source	Kind	Error Structure
1,*f*	fishery or survey *f*	CPUE or abundance index	lognormal
2,*f*	fishery *f*	Discard biomass	normal
3,*f*	fishery or survey *f*	Mean body weight	normal
4,*f*	fishery or survey *f*	Length-composition	multinomial
5,*f*	fishery or survey *f*	Age-composition	multinomial
6,*f*	fishery or survey *f*	Mean size-at-age	normal
7,f	Fishery – all	Initial equilibrium catch	normal
R		Recruitment deviations	lognormal
P		Random parameter time-series deviations	normal
Θ		Parameter priors	Normal or Beta
	Fishery – all	Negative abundance penalty	N/A

Table A.2 Sequence of calculations in the multi-stage forecast used in Stock Synthesis

1. Stage 1, for each year of forecast and with no recruitment deviations
   a. Conditions
      i. $F = F_{\text{lim}}$
      ii. Fixed input catch amounts ignored
      iii. No catch adjustments (caps and allocations)
      iv. No implementation error
   b. Result: OFL conditioned on catching OFL each year
2. Stage 2, for each year of forecast and with no recruitment deviations
   a. Conditions, first calculation
      i. $F = F_{\text{lim}}$
      ii. Fixed input catch amounts ignored
      iii. No catch adjustments (caps and allocations)
      iv. No implementation error
   b. First result: OFL catch conditioned on catching ABC previous year. Stored in std_vector
   c. Conditions, second calculation
      i. $F = F_{\text{tgt}}$, e.g. the harvest policy, to calculate the target catch for each fleet in each season
      ii. Fixed input catch amounts replace calculated target catch amounts
      iii. Catch adjustments (caps and allocations) applied on annual basis (after looping through seasons and areas within this year). These adjustments utilize the logistic joiner approach common in SS so the overall results remain differentiable
      iv. No implementation error
   d. Second result: ABC as adjusted for caps and allocations
   e. Conditions, third calculation
      i. No implementation error, still using no recruitment deviations
      ii. *F* recalculated to match adjusted catches from calculation step 2
   f. Third result: survivors to pass to the next year in the stage 2 calculations.
3. Stage 3, recruitment deviations and implementation error now active parameters. For each year:
   a. Catches from Stage 2 multiplied by the random term for implementation error
      i. *F* adjusted to match the catch*error while taking into account the population abundance that now has recruitment deviations. This is most easily visualized in a MCMC context where the recruitment deviation and the implementation error deviations take on non-zero values in each instance. In MLE, because the forecast recruitments and implementation error are estimated parameters with variance, their variance still propagates to the derived quantities in the forecast.
   b. Result: Values for *F*, *SSB*, Recruitment, Catch are stored in std-vectors
   c. In addition, the ratios F/F_{lim} and SSB/SSB_{lim} or SSB/SSB_{tgt} are also stored in std_vectors.
   d. Estimated variance in these ratios allows calculation of annual probability that $F>F_{\text{lim}}$ or $B<B_{\text{lim}}$. This is essentially the realized P* conditioned on the specified harvest policy.

Figures

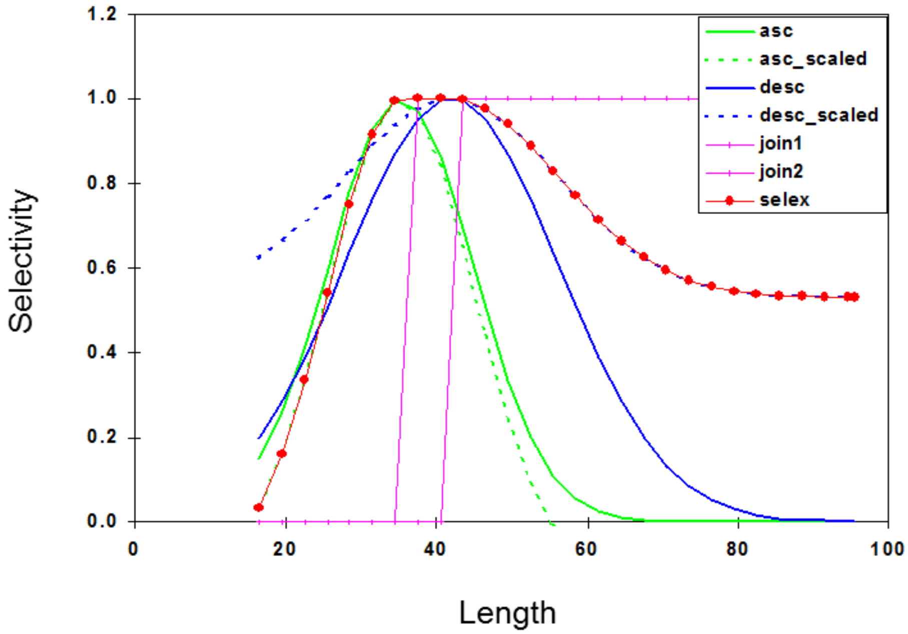

Figure A.1 Realized double normal selectivity (red) composed from the ascending, descending, and joiner sections.

Appendix B: Stocks which are currently assessed using Stock Synthesis (version 3) within the U.S. and internationally.

Species	Region	Assessment Author and Year
United States		
Arrowtooth flounder	Pacific Coast	Kaplan and Hesler 2007
California halibut	Pacific Coast	Maunder et al. 2011
Canary rockfish	Pacific Coast	Stewart 2009
Darkblotched rockfish	Pacific Coast	Stephens et al. 2011
Dover sole	Pacific Coast	Hicks and Wetzel 2011
English sole	Pacific Coast	Stewart 2008
Greenspotted rockfish	Pacific Coast	Dick et al. 2011
Greenstriped rockfish	Pacific Coast	Hicks et al. 2009
Lingcod	Pacific Coast	Hamel et al. 2009
Longnose skate	Pacific Coast	Gertseva and Schirripa 2008
Pacific hake	Pacific Ocean (U.S and Canada)	International Joint Technical Committee for Pacific hake 2012
Pacific ocean perch	Pacific Coast	Hamel and Ono 2011
Pacific mackerel	Pacific Coast	Crone et al. 2009
Pacific sardine	Pacific Coast	Hill et al. 2011
Petrale sole	Pacific Coast	Haltuch et al. 2011
Sablefish	Pacific Coast	Stewart et al. 2011
Shortbelly rockfish	Pacific Coast	Field et al. 2007
Spiny dogfish	Pacific Coast	Gertseva and Taylor 2011
Splitnose rockfish	Pacific Coast	Gertseva et al. 2009
Widow rockfish	Pacific Coast	He et al. 2011
Yelloweye rockfish	Pacific Coast	Taylor and Wetzel 2011
Black rockfish	Southern Pacific Coast	Sampson 2008
Blackgill rockfish	Southern Pacific Coast	Field and Pearson 2011
Blue rockfish	Southern Pacific Coast	Key et al. 2008
Bocaccio rockfish	Southern Pacific Coast	Field 2011
Chilipepper rockfish	Southern Pacific Coast	Field 2008
Cowcod rockfish	Southern Pacific Coast	Dick et al. 2008
Black rockfish	Northern Pacific Coast	Wallace et al. 2008
Cabezon	Northern Pacific Coast	Cope and Key 2009
Alaska Skate	Bering Sea/Aleutian Islands	Ormseth and Matta 2011
Greenland turbot	Bering Sea/Aleutian Islands	Ianelli et al. 2011
Pacific cod	Bering Sea/Aleutian Islands	Thompson and Lauth 2011
Pacific cod	Gulf of Alaska	Thompson et al. 2011
Tilefish	Gulf of Mexico	SEDAR 2011
Yellowedge grouper	Gulf of Mexico	SEDAR 2011
Tuna/Billfish		
Bigeye tuna	Eastern Pacific Ocean	Aires-da-Silva and Maunder 2012
Yellowfin tuna	Eastern Pacific Ocean	Aires-da-Silva and Maunder 2012
Striped marlin	Eastern Pacific Ocean	Hinton and Maunder 2010
Swordfish	Eastern Pacific Ocean	Hinton and Maunder 2011

Albacore	North Pacific Ocean	International Scientific Committee for Tuna and Tuna-like Species in the North Pacific Ocean 2011
Albacore	Atlantic Ocean	ICCAT 2010
Blue marlin	Atlantic Ocean	ICCAT 2011
Bigeye tuna	Indian Ocean	Kolody et al. 2010
Skipjack tuna	Indian Ocean	Kolody et al. 2011
Swordfish	Indian Ocean	Kolody and Herrera 2011
European		
Anglerfish	North Atlantic	ICES 2012b
Iberian sardine	North Atlantic	ICES 2012a
Northern hake	North Atlantic	ICES 2010
White Anglerfish	North Atlantic	ICES 2012b
Australian		
Blue grenadier	South East Australia	Tuck et al. 2011
Eastern gemfish	South East Australia	Little and Rowling 2011
Jackass Morwong	South East Australia	Wayte 2011
Orange roughy (Cascade Plateau Stock)	South East Australia	Wayte and Bax 2007
Pink ling (western)	South East Australia	Taylor 2011
Pink ling (eastern)	South East Australia	Taylor 2011
School whiting	South East Australia	Day 2010
Silver warehou	South East Australia	Tuck and Fay 2009
Tiger flathead	South East Australia	Klaer 2010
Bight redfish	Great Australian Bight	Klaer 2010
Deepwater flathead	Great Australian Bight	Klaer 2010
Patagonian toothfish	Macquarie Island	Wayte and Fay 2012

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